



SEQUENCE LISTING

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<120> A BINDING MOTIF OF A RECEPTOR

<130> 3991/0K379

<140> US 10/099,895

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<151> 2000-09-15

<160> 47

<170> PatentIn version 3.1

<210> 1

<211> 897

<212> PRT

<213> Homo sapiens

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Met Val Leu Ala Gln Gly Leu Leu Ser Met Ala Leu Leu Ala Leu Cys
1 5 10 15

Trp Glu Arg Ser Leu Ala Gly Ala Glu Glu Thr Ile Pro Leu Gln Thr
20 25 30

Leu Arg Cys Tyr Asn Asp Tyr Thr Ser His Ile Thr Cys Arg Trp Ala
35 40 45

Asp Thr Gln Asp Ala Gln Arg Leu Val Asn Val Thr Leu Ile Arg Arg
50 55 60

Val Asn Glu Asp Leu Leu Glu Pro Val Ser Cys Asp Leu Ser Asp Asp
65 70 75 80

Met Pro Trp Ser Ala Cys Pro His Pro Arg Cys Val Pro Arg Arg Cys
85 90 95

Val Ile Pro Cys Gln Ser Phe Val Val Thr Asp Val Asp Tyr Phe Ser
100 105 110

Phe Gln Pro Asp Arg Pro Leu Gly Thr Arg Leu Thr Val Thr Leu Thr

115

120

125

Gln His Val Gln Pro Pro Glu Pro Arg Asp Leu Gln Ile Ser Thr Asp
 130 135 140

Gln Asp His Phe Leu Leu Thr Trp Ser Val Ala Leu Gly Ser Pro Gln
 145 150 155 160

Ser His Trp Leu Ser Pro Gly Asp Leu Glu Phe Glu Val Val Tyr Lys
 165 170 175

Arg Leu Gln Asp Ser Trp Glu Asp Ala Ala Ile Leu Leu Ser Asn Thr
 180 185 190

Ser Gln Ala Thr Leu Gly Pro Glu His Leu Met Pro Ser Ser Thr Tyr
 195 200 205

Val Ala Arg Val Arg Thr Arg Leu Ala Pro Gly Ser Arg Leu Ser Gly
 210 215 220

Arg Pro Ser Lys Trp Ser Pro Glu Val Cys Trp Asp Ser Gln Pro Gly
 225 230 235 240

Asp Glu Ala Gln Pro Gln Asn Leu Glu Cys Phe Phe Asp Gly Ala Ala
 245 250 255

Val Leu Ser Cys Ser Trp Glu Val Arg Lys Glu Val Ala Ser Ser Val
 260 265 270

Ser Phe Gly Leu Phe Tyr Lys Pro Ser Pro Asp Ala Gly Glu Glu Glu
 275 280 285

Cys Ser Pro Val Leu Arg Glu Gly Leu Gly Ser Leu His Thr Arg His
 290 295 300

His Cys Gln Ile Pro Val Pro Asp Pro Ala Thr His Gly Gln Tyr Ile
 305 310 315 320

Val Ser Val Gln Pro Arg Arg Ala Glu Lys His Ile Lys Ser Ser Val
 325 330 335

Asn Ile Gln Met Ala Pro Pro Ser Leu Asn Val Thr Lys Asp Gly Asp
 340 345 350

Ser Tyr Ser Leu Arg Trp Glu Thr Met Lys Met Arg Tyr Glu His Ile
355 360 365

Asp His Thr Phe Glu Ile Gln Tyr Arg Lys Asp Thr Ala Thr Trp Lys
370 375 380

Asp Ser Lys Thr Glu Thr Leu Gln Asn Ala His Ser Met Ala Leu Pro
385 390 395 400

Ala Leu Glu Pro Ser Thr Arg Tyr Trp Ala Arg Val Arg Val Arg Thr
405 410 415

Ser Arg Thr Gly Tyr Asn Gly Ile Trp Ser Glu Trp Ser Glu Ala Arg
420 425 430

Ser Trp Asp Thr Glu Ser Val Leu Pro Met Trp Val Leu Ala Leu Ile
435 440 445

Val Ile Phe Leu Thr Ile Ala Val Leu Leu Ala Leu Arg Phe Cys Gly
450 455 460

Ile Tyr Gly Tyr Arg Leu Arg Arg Lys Trp Glu Glu Lys Ile Pro Asn
465 470 475 480

Pro Ser Lys Ser His Leu Phe Gln Asn Gly Ser Ala Glu Leu Trp Pro
485 490 495

Pro Gly Ser Met Ser Ala Phe Thr Ser Gly Ser Pro Pro His Gln Gly
500 505 510

Pro Trp Gly Ser Arg Phe Pro Glu Leu Glu Gly Val Phe Pro Val Gly
515 520 525

Phe Gly Asp Ser Glu Val Ser Pro Leu Thr Ile Glu Asp Pro Lys His
530 535 540

Val Cys Asp Pro Pro Ser Gly Pro Asp Thr Thr Pro Ala Ala Ser Asp
545 550 555 560

Leu Pro Thr Glu Gln Pro Pro Ser Pro Gln Pro Gly Pro Pro Ala Ala
565 570 575

Ser His Thr Pro Glu Lys Gln Ala Ser Ser Phe Asp Phe Asn Gly Pro
580 585 590

Tyr Leu Gly Pro Pro His Ser Arg Ser Leu Pro Asp Ile Leu Gly Gln
595 600 605

Pro Glu Pro Pro Gln Glu Gly Gly Ser Gln Lys Ser Pro Pro Pro Gly
610 615 620

Ser Leu Glu Tyr Leu Cys Leu Pro Ala Gly Gly Gln Val Gln Leu Val
625 630 635 640

Pro Leu Ala Gln Ala Met Gly Pro Gly Gln Ala Val Glu Val Glu Arg
645 650 655

Arg Pro Ser Gln Gly Ala Ala Gly Ser Pro Ser Leu Glu Ser Gly Gly
660 665 670

Gly Pro Ala Pro Pro Ala Leu Gly Pro Arg Val Gly Gly Gln Asp Gln
675 680 685

Lys Asp Ser Pro Val Ala Ile Pro Met Ser Ser Gly Asp Thr Glu Asp
690 695 700

Pro Gly Val Ala Ser Gly Tyr Val Ser Ser Ala Asp Leu Val Phe Thr
705 710 715 720

Pro Asn Ser Gly Ala Ser Ser Val Ser Leu Val Pro Ser Leu Gly Leu
725 730 735

Pro Ser Asp Gln Thr Pro Ser Leu Cys Pro Gly Leu Ala Ser Gly Pro
740 745 750

Pro Gly Ala Pro Gly Pro Val Lys Ser Gly Phe Glu Gly Tyr Val Glu
755 760 765

Leu Pro Pro Ile Glu Gly Arg Ser Pro Arg Ser Pro Arg Asn Asn Pro
770 775 780

Val Pro Pro Glu Ala Lys Ser Pro Val Leu Asn Pro Gly Glu Arg Pro
785 790 795 800

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<223> "X" is any amino acid

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<222> (5)..(5)
<223> "X" is any amino acid

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<222> (4)..(4)
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<400> 3

Arg Ser Xaa Ser Xaa Pro
1 5

<210> 4
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<212> PRT
<213> Homo sapiens

<400> 4

His Ser Arg Ser Leu Pro
1 5

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<213> Homo sapiens

<400> 5

Ser Ser Ser Arg Pro
1 5

<210> 6
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<212> PRT
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<400> 6

Ser Asn Ser Lys Pro
1 5

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Ala Asp Val Ser Pro Thr Ser Pro Gln Pro Glu Gly Leu Leu Val Leu
805 810 815

Gln Gln Val Gly Asp Tyr Cys Phe Leu Pro Gly Leu Gly Pro Gly Pro
820 825 830

Leu Ser Leu Arg Ser Lys Pro Ser Ser Pro Gly Pro Gly Pro Glu Ile
835 840 845

Lys Asn Leu Asp Gln Ala Phe Gln Val Lys Lys Pro Pro Gly Gln Ala
850 855 860

Val Pro Gln Val Pro Val Ile Gln Leu Phe Lys Ala Leu Lys Gln Gln
865 870 875 880

Asp Tyr Leu Ser Leu Pro Pro Trp Glu Val Asn Lys Pro Gly Glu Val
885 890 895

Cys

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Ser Asp Ser Ser Pro
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Ser Ile Ser Ala Pro
1 5

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Ser Leu Ser Leu Pro
1 5

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Ser Ala Ser Thr Pro
1 5

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Ser Pro Ser Phe Pro
1 5

<210> 12
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<213> Homo sapiens

<400> 12

Ser Asn Ser Gln Pro
1 5

<210> 13

<211> 5

<212> PRT

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<400> 13

Ser Val Ser Ser Pro
1 5

<210> 14

<211> 5

<212> PRT

<213> Homo sapiens

<400> 14

Ser Thr Ser Val Pro
1 5

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<212> PRT

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<400> 15

Ser Lys Ser Pro Pro
1 5

<210> 16

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<212> PRT

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<400> 16

Ser Arg Ser Gln Pro
1 5

<210> 17

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<212> PRT

<213> Homo sapiens

<400> 17

Ser Ser Ser Leu Pro
1 5

<210> 18

<211> 5

<212> PRT

<213> Homo sapiens

<400> 18

Ser Ser Ser Gly Pro
1 5

<210> 19

<211> 5

<212> PRT

<213> Homo sapiens

<400> 19

Ser Ser Ser Phe Pro
1 5

<210> 20

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Ser Pro Ser Tyr Pro
1 5

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Ser Gly Ser Leu Pro
1 5

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Ser Gln Ser Ser Pro
1 5

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Ser Pro Ser Leu Pro
1 5

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Ser Gly Ser Thr Pro
1 5

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Ser Val Ser Pro Pro
1 5

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Ser Gly Ser Gly Pro
1 5

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Ser Leu Gly Ser Ser Pro
1 5

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<212> PRT
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Ser Ser Ser Gln Pro
1 5

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<213> Homo sapiens

<400> 29

Lys Ser Ser Glu Arg Thr Pro
1 5

<210> 30
<211> 7
<212> PRT
<213> Homo sapiens

<400> 30

Lys Ser Ser Glu Ser Thr Pro
1 5

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His Ser Arg Ser Leu Pro
1 5

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<211> 976
<212> PRT
<213> Homo sapiens

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Met Arg Gly Ala Arg Gly Ala Trp Asp Phe Leu Cys Val Leu Leu Leu
1 . 5 10 15

Leu Leu Arg Val Gln Thr Gly Ser Ser Gln Pro Ser Val Ser Pro Gly
20 25 30

Glu Pro Ser Pro Pro Ser Ile His Pro Gly Lys Ser Asp Leu Ile Val
35 40 45

Arg Val Gly Asp Glu Ile Arg Leu Leu Cys Thr Asp Pro Gly Phe Val
50 55 60

Lys Trp Thr Phe Glu Ile Leu Asp Glu Thr Asn Glu Asn Lys Gln Asn
65 70 75 80

Glu Trp Ile Thr Glu Lys Ala Glu Ala Thr Asn Thr Gly Lys Tyr Thr
85 90 95

Cys Thr Asn Lys His Gly Leu Ser Asn Ser Ile Tyr Val Phe Val Arg
100 105 110

Asp Pro Ala Lys Leu Phe Leu Val Asp Arg Ser Leu Tyr Gly Lys Glu
115 120 125

Asp Asn Asp Thr Leu Val Arg Cys Pro Leu Thr Asp Pro Glu Val Thr
130 135 140

Asn Tyr Ser Leu Lys Gly Cys Gln Gly Lys Pro Leu Pro Lys Asp Leu
145 150 155 160

Arg Phe Ile Pro Asp Pro Lys Ala Gly Ile Met Ile Lys Ser Val Lys
165 170 175

Arg Ala Tyr His Arg Leu Cys Leu His Cys Ser Val Asp Gln Glu Gly
180 185 190

Lys Ser Val Leu Ser Glu Lys Phe Ile Leu Lys Val Arg Pro Ala Phe
195 200 205

Lys Ala Val Pro Val Val Ser Val Ser Lys Ala Ser Tyr Leu Leu Arg
210 215 220

Glu Gly Glu Glu Phe Thr Val Thr Cys Thr Ile Lys Asp Val Ser Ser
225 230 235 240

Ser Val Tyr Ser Thr Trp Lys Arg Glu Asn Ser Gln Thr Lys Leu Gln
245 250 255

Glu Lys Tyr Asn Ser Trp His His Gly Asp Phe Asn Tyr Glu Arg Gln
260 265 270

Ala Thr Leu Thr Ile Ser Ser Ala Arg Val Asn Asp Ser Gly Val Phe
275 280 285

Met Cys Tyr Ala Asn Asn Thr Phe Gly Ser Ala Asn Val Thr Thr Thr
290 295 300

Leu Glu Val Val Asp Lys Gly Phe Ile Asn Ile Phe Pro Met Ile Asn
305 310 315 320

Thr Thr Val Phe Val Asn Asp Gly Glu Asn Val Asp Leu Ile Val Glu
325 330 335

Tyr Glu Ala Phe Pro Lys Pro Glu His Gln Gln Trp Ile Tyr Met Asn
340 345 350

Arg Thr Phe Thr Asp Lys Trp Glu Asp Tyr Pro Lys Ser Glu Asn Glu
355 360 365

Ser Asn Ile Arg Tyr Val Ser Glu Leu His Leu Thr Arg Leu Lys Gly
370 375 380

Thr Glu Gly Gly Thr Tyr Thr Phe Leu Val Ser Asn Ser Asp Val Asn
385 390 395 400

Ala Ala Ile Ala Phe Asn Val Tyr Val Asn Thr Lys Pro Glu Ile Leu
405 410 415

Thr Tyr Asp Arg Leu Val Asn Gly Met Leu Gln Cys Val Ala Ala Gly
420 425 430

Phe Pro Glu Pro Thr Ile Asp Trp Tyr Phe Cys Pro Gly Thr Glu Gln
435 440 445

Arg Cys Ser Ala Ser Val Leu Pro Val Asp Val Gln Thr Leu Asn Ser
 450 455 460

Ser Gly Pro Pro Phe Gly Lys Leu Val Val Gln Ser Ser Ile Asp Ser
 465 470 475 480

Ser Ala Phe Lys His Asn Gly Thr Val Glu Cys Lys Ala Tyr Asn Asp
 485 490 495

Val Gly Lys Thr Ser Ala Tyr Phe Asn Phe Ala Phe Lys Gly Asn Asn
 500 505 510

Lys Glu Gln Ile His Pro His Thr Leu Phe Thr Pro Leu Leu Ile Gly
 515 520 525

Phe Val Ile Val Ala Gly Met Met Cys Ile Ile Val Met Ile Leu Thr
 530 535 540

Tyr Lys Tyr Leu Gln Lys Pro Met Tyr Glu Val Gln Trp Lys Val Val
 545 550 555 560

Glu Glu Ile Asn Gly Asn Asn Tyr Val Tyr Ile Asp Pro Thr Gln Leu
 565 570 575

Pro Tyr Asp His Lys Trp Glu Phe Pro Arg Asn Arg Leu Ser Phe Gly
 580 585 590

Lys Thr Leu Gly Ala Gly Ala Phe Gly Lys Val Val Glu Ala Thr Ala
 595 600 605

Tyr Gly Leu Ile Lys Ser Asp Ala Ala Met Thr Val Ala Val Lys Met
 610 615 620

Leu Lys Pro Ser Ala His Leu Thr Glu Arg Glu Ala Leu Met Ser Glu
 625 630 635 640

Leu Lys Val Leu Ser Tyr Leu Gly Asn His Met Asn Ile Val Asn Leu
 645 650 655

Leu Gly Ala Cys Thr Ile Gly Gly Pro Thr Leu Val Ile Thr Glu Tyr
 660 665 670

Cys Cys Tyr Gly Asp Leu Leu Asn Phe Leu Arg Arg Lys Arg Asp Ser

675	680	685
Phe Ile Cys Ser Lys Gln Glu Asp His Ala Glu Ala Ala Leu Tyr Lys 690 695 700		
Asn Leu Leu His Ser Lys Glu Ser Ser Cys Ser Asp Ser Thr Asn Glu 705 710 715 720		
Tyr Met Asp Met Lys Pro Gly Val Ser Tyr Val Val Pro Thr Lys Ala 725 730 735		
Asp Lys Arg Arg Ser Val Arg Ile Gly Ser Tyr Ile Glu Arg Asp Val 740 745 750		
Thr Pro Ala Ile Met Glu Asp Asp Glu Leu Ala Leu Asp Leu Glu Asp 755 760 765		
Leu Leu Ser Phe Ser Tyr Gln Val Ala Lys Gly Met Ala Phe Leu Ala 770 775 780		
Ser Lys Asn Cys Ile His Arg Asp Leu Ala Ala Arg Asn Ile Leu Leu 785 790 795 800		
Thr His Gly Arg Ile Thr Lys Ile Cys Asp Phe Gly Leu Ala Arg Asp 805 810 815		
Ile Lys Asn Asp Ser Asn Tyr Val Val Lys Gly Asn Ala Arg Leu Pro 820 825 830		
Val Lys Trp Met Ala Pro Glu Ser Ile Phe Asn Cys Val Tyr Thr Phe 835 840 845		
Glu Ser Asp Val Trp Ser Tyr Gly Ile Phe Leu Trp Glu Leu Phe Ser 850 855 860		
Leu Gly Ser Ser Pro Tyr Pro Gly Met Pro Val Asp Ser Lys Phe Tyr 865 870 875 880		
Lys Met Ile Lys Glu Gly Phe Arg Met Leu Ser Pro Glu His Ala Pro 885 890 895		
Ala Glu Met Tyr Asp Ile Met Lys Thr Cys Trp Asp Ala Asp Pro Leu 900 905 910		

Lys Arg Pro Thr Phe Lys Gln Ile Val Gln Leu Ile Glu Lys Gln Ile
915 920 925

Ser Glu Ser Thr Asn His Ile Tyr Ser Asn Leu Ala Asn Cys Ser Pro
930 935 940

Asn Arg Gln Lys Pro Val Val Asp His Ser Val Arg Ile Asn Ser Val
945 950 955 960

Gly Ser Thr Ala Ser Ser Ser Gln Pro Leu Leu Val His Asp Asp Val
965 970 975

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<400> 33

Met Pro Ser Trp Ala Leu Phe Met Val Thr Ser Cys Leu Leu Leu Ala
1 5 10 15

Pro Gln Asn Leu Ala Gln Val Ser Ser Gln Asp Val Ser Leu Leu Ala
20 25 30

Ser Asp Ser Glu Pro Leu Lys Cys Phe Ser Arg Thr Phe Glu Asp Leu
35 40 45

Thr Cys Phe Trp Asp Glu Glu Glu Ala Ala Pro Ser Gly Thr Tyr Gln
50 55 60

Leu Leu Tyr Ala Tyr Pro Arg Glu Lys Pro Arg Ala Cys Pro Leu Ser
65 70 75 80

Ser Gln Ser Met Pro His Phe Gly Thr Arg Tyr Val Cys Gln Phe Pro
85 90 95

Asp Gln Glu Glu Val Arg Leu Phe Phe Pro Leu His Leu Trp Val Lys
100 105 110

Asn Val Phe Leu Asn Gln Thr Arg Thr Gln Arg Val Leu Phe Val Asp
115 120 125

Ser Val Gly Leu Pro Ala Pro Pro Ser Ile Ile Lys Ala Met Gly Gly
130 135 140

Ser Gln Pro Gly Glu Leu Gln Ile Ser Trp Glu Glu Pro Ala Pro Glu
145 150 155 160

Ile Ser Asp Phe Leu Arg Tyr Glu Leu Arg Tyr Gly Pro Arg Asp Pro
165 170 175

Lys Asn Ser Thr Gly Pro Thr Val Ile Gln Leu Ile Ala Thr Glu Thr
180 185 190

Cys Cys Pro Ala Leu Gln Arg Pro His Ser Ala Ser Ala Leu Asp Gln
195 200 205

Ser Pro Cys Ala Gln Pro Thr Met Pro Trp Gln Asp Gly Pro Lys Gln
210 215 220

Thr Ser Pro Ser Arg Glu Ala Ser Ala Leu Thr Ala Glu Gly Gly Ser
225 230 235 240

Cys Leu Ile Ser Gly Leu Gln Pro Gly Asn Ser Tyr Trp Leu Gln Leu
245 250 255

Arg Ser Glu Pro Asp Gly Ile Ser Leu Gly Gly Ser Trp Gly Ser Trp
260 265 270

Ser Leu Pro Val Thr Val Asp Leu Pro Gly Asp Ala Val Ala Leu Gly
275 280 285

Leu Gln Cys Phe Thr Leu Asp Leu Lys Asn Val Thr Cys Gln Trp Gln
290 295 300

Gln Gln Asp His Ala Ser Ser Gln Gly Phe Phe Tyr His Ser Arg Ala
305 310 315 320

Arg Cys Cys Pro Arg Asp Arg Tyr Pro Ile Trp Glu Asn Cys Glu Glu
325 330 335

Glu Glu Lys Thr Asn Pro Gly Leu Gln Thr Pro Gln Phe Ser Arg Cys
340 345 350

His Phe Lys Ser Arg Asn Asp Ser Ile Ile His Ile Leu Val Glu Val

355

360

365

Thr Thr Ala Pro Gly Thr Val His Ser Tyr Leu Gly Ser Pro Phe Trp
 370 375 380

Ile His Gln Ala Val Arg Leu Pro Thr Pro Asn Leu His Trp Arg Glu
 385 390 395 400

Ile Ser Ser Gly His Leu Glu Leu Glu Trp Gln His Pro Ser Ser Trp
 405 410 415

Ala Ala Gln Glu Thr Cys Tyr Gln Leu Arg Tyr Thr Gly Glu Gly His
 420 425 430

Gln Asp Trp Lys Val Leu Glu Pro Pro Leu Gly Ala Arg Gly Gly Thr
 435 440 445

Leu Glu Leu Arg Pro Arg Ser Arg Tyr Arg Leu Gln Leu Arg Ala Arg
 450 455 460

Leu Asn Gly Pro Thr Tyr Gln Gly Pro Trp Ser Ser Trp Ser Asp Pro
 465 470 475 480

Thr Arg Val Glu Thr Ala Thr Glu Thr Ala Trp Ile Ser Leu Val Thr
 485 490 495

Ala Leu His Leu Val Leu Gly Leu Ser Ala Val Leu Gly Leu Leu Leu
 500 505 510

Leu Arg Trp Gln Phe Pro Ala His Tyr Arg Arg Leu Arg His Ala Leu
 515 520 525

Trp Pro Ser Leu Pro Asp Leu His Arg Val Leu Gly Gln Tyr Leu Arg
 530 535 540

Asp Thr Ala Ala Leu Ser Pro Pro Lys Ala Thr Val Ser Asp Thr Cys
 545 550 555 560

Glu Glu Val Glu Pro Ser Leu Leu Glu Ile Leu Pro Lys Ser Ser Glu
 565 570 575

Arg Thr Pro Leu Pro Leu Cys Ser Ser Gln Ala Gln Met Asp Tyr Arg
 580 585 590

Arg Leu Gln Pro Ser Cys Leu Gly Thr Met Pro Leu Ser Val Cys Pro
595 600 605

Pro Met Ala Glu Ser Gly Ser Cys Cys Thr Thr His Ile Ala Asn His
610 615 620

Ser Tyr Leu Pro Leu Ser Tyr Trp Gln Gln Pro
625 630 635

<210> 34
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Met Pro Ser Trp Ala Leu Phe Met Val Thr Ser Cys Leu Leu Leu Ala
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Leu Pro Asn Gln Ala Gln Val Thr Ser Gln Asp Val Phe Leu Leu Ala
20 25 30

Leu Gly Thr Glu Pro Leu Asn Cys Phe Ser Gln Thr Phe Glu Asp Leu
35 40 45

Thr Cys Phe Trp Asp Glu Glu Glu Ala Ala Pro Ser Gly Thr Tyr Gln
50 55 60

Leu Leu Tyr Ala Tyr Arg Gly Glu Lys Pro Arg Ala Cys Pro Leu Tyr
65 70 75 80

Ser Gln Ser Val Pro Thr Phe Gly Thr Arg Tyr Val Cys Gln Phe Pro
85 90 95

Ala Gln Asp Glu Val Arg Leu Phe Phe Pro Leu His Leu Trp Val Lys
100 105 110

Asn Val Ser Leu Asn Gln Thr Leu Ile Gln Arg Val Leu Phe Val Asp
115 120 125

Ser Val Gly Leu Pro Ala Pro Pro Arg Val Ile Lys Ala Arg Gly Gly
130 135 140

Ser Gln Pro Gly Glu Leu Gln Ile His Trp Glu Ala Pro Ala Pro Glu
 145 150 155 160

Ile Ser Asp Phe Leu Arg His Glu Leu Arg Tyr Gly Pro Thr Asp Ser
 165 170 175

Ser Asn Ala Thr Ala Pro Ser Val Ile Gln Leu Leu Ser Thr Glu Thr
 180 185 190

Cys Cys Pro Thr Leu Trp Met Pro Asn Pro Val Pro Val Leu Asp Gln
 195 200 205

Pro Pro Cys Val His Pro Thr Ala Ser Gln Pro His Gly Pro Ala Pro
 210 215 220

Phe Leu Thr Val Lys Gly Gly Ser Cys Leu Val Ser Gly Leu Gln Ala
 225 230 235 240

Ser Lys Ser Tyr Trp Leu Gln Leu Arg Ser Gln Pro Asp Gly Val Ser
 245 250 255

Leu Arg Gly Ser Trp Gly Pro Trp Ser Phe Pro Val Thr Val Asp Leu
 260 265 270

Pro Gly Asp Ala Val Thr Ile Gly Leu Gln Cys Phe Thr Leu Asp Leu
 275 280 285

Lys Met Val Thr Cys Gln Trp Gln Gln Gln Asp Arg Thr Ser Ser Gln
 290 295 300

Gly Phe Phe Arg His Ser Arg Thr Arg Cys Cys Pro Thr Asp Arg Asp
 305 310 315 320

Pro Thr Trp Glu Lys Cys Glu Glu Glu Glu Pro Arg Pro Gly Ser Gln
 325 330 335

Pro Ala Leu Val Ser Arg Cys His Phe Lys Ser Arg Asn Asp Ser Val
 340 345 350

Ile His Ile Leu Val Glu Val Thr Thr Ala Gln Gly Ala Val His Ser
 355 360 365

Tyr Leu Gly Ser Pro Phe Trp Ile His Gln Ala Val Leu Leu Pro Thr

370

375

380

Pro Ser Leu His Trp Arg Glu Val Ser Ser Gly Arg Leu Glu Leu Glu
 385 390 395 400

Trp Gln His Gln Ser Ser Trp Ala Ala Gln Glu Thr Cys Tyr Gln Leu
 405 410 415

Arg Tyr Thr Gly Glu Gly Arg Glu Asp Trp Lys Val Leu Glu Pro Ser
 420 425 430

Leu Gly Ala Arg Gly Gly Thr Leu Glu Leu Arg Pro Arg Ala Arg Tyr
 435 440 445

Ser Leu Gln Leu Arg Ala Arg Leu Asn Gly Pro Thr Tyr Gln Gly Pro
 450 455 460

Trp Ser Ala Trp Ser Pro Pro Ala Arg Val Ser Thr Gly Ser Glu Thr
 465 470 475 480

Ala Trp Ile Thr Leu Val Thr Ala Leu Leu Leu Val Leu Ser Leu Ser
 485 490 495

Ala Leu Leu Gly Leu Leu Leu Leu Lys Trp Gln Phe Pro Ala His Tyr
 500 505 510

Arg Arg Leu Arg His Ala Leu Trp Pro Ser Leu Pro Asp Leu His Arg
 515 520 525

Val Leu Gly Gln Tyr Leu Arg Asp Thr Ala Ala Leu Ser Pro Ser Lys
 530 535 540

Ala Thr Val Thr Asp Ser Cys Glu Glu Val Glu Pro Ser Leu Leu Glu
 545 550 555 560

Ile Leu Pro Lys Ser Ser Glu Ser Thr Pro Leu Pro Leu Cys Pro Ser
 565 570 575

Gln Pro Gln Met Asp Tyr Arg Gly Leu Gln Pro Cys Leu Arg Thr Met
 580 585 590

Pro Leu Ser Val Cys Pro Pro Met Ala Glu Thr Gly Ser Cys Cys Thr
 595 600 605

Thr His Ile Ala Asn His Ser Tyr Leu Pro Leu Ser Tyr Trp Gln Gln
610 615 620

Pro
625

<210> 35
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<223> represents residues 581 to 587

<400> 35

Pro His Ser Arg Ser Leu Pro
1 5

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Gly Glu Phe Ala Ala Ala Ala
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Arg Ser Lys Pro Ser Ser Pro
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<210> 38
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Glu Phe Ala Ala Ala Ala Ala
1 5

<210> 39
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<213> Homo sapiens

<400> 39

Cys Leu Gly Pro Pro His Ser Arg Ser Leu Pro Asp Ile Leu Gly
1 5 10 15

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<400> 40

Cys Leu Ser Gln Arg Gln Arg Ser Thr Ser Thr Pro Asn Val His Met
1 5 10 15

<210> 41
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Cys Pro Leu Ser Leu Arg Ser Lys Pro Ser Pro Gly Pro Gly Pro
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Cys Leu Pro Leu Ser Gly Pro Asp Ser His Ile Arg Gly Pro Leu
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Glu Phe Ala Ala Ala Ala
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Arg Ser Leu
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Ala Ala Ala
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<223> "X" is any amino acid

<220>
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<223> representing residues 585 to 588 of the GM-CSF/IL-3/IL-5 receptor

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Ser Xaa Xaa Asp
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<212> PRT

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<223> representing residues 582 to 585 of the GM-CSF/IL-3/IL-5 receptor

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His Ser Arg Ser
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